

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: February 23, 2003, 21:05:35 : Search time 3922 Seconds  
(without alignments)  
10907.987 Million cell updates/sec

Title: US-09-725-010-1  
Perfect score: 1470  
Sequence: 1 ggaatctctttttcttttc.....cttttagtttgcgaatatg 1470

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg\_hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pin.\*  
35: em.htg\_rod.\*  
36: em.htg\_mam.\*  
37: em.htg\_vrt.\*  
38: em.sy.\*  
39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1470	100.0	1470	6	AX154641	AX154641 Sequence
2	505	34.4	2682	8	CAU64206	U64206 Candida alb
3	153	10.4	2188	8	AF001978	AF001978 Candida a
c 4	136.2	9.3	42565	8	CAC33A5	AL033396 C.albican
c 5	91.2	6.2	86827	3	PFMAL3P5	AL034556 Plasmodiu
6	86.8	5.9	104992	2	AC005504	AC005504 Plasmodiu
7	86.8	5.9	169546	2	AC004157	AC004157 Plasmodiu
c 8	75.2	5.1	104014	2	AC116921	AC116921 Dictyoste
9	73.4	5.0	14867	3	AE001398	AE001398 Plasmodiu
10	73.4	5.0	164399	3	PFMAL3P6	Z98551 Plasmodium
11	72.8	5.0	113880	3	PFMAL3P4	AL008970 Plasmodiu
c 12	70.8	4.8	2009	6	AX457067	AX457067 Sequence
c 13	70.4	4.8	192929	2	AC005505	AC005505 Plasmodiu
14	69.4	4.7	56099	2	AC115598	AC115598 Dictyoste
15	69.2	4.7	253305	3	PFMAL3P7	AL034559 Plasmodiu
c 16	68.2	4.6	115489	2	AC117072	AC117072 Dictyoste
c 17	68	4.6	9810	6	AX345328	AX345328 Sequence
18	67.2	4.6	7347	1	AF211124	AF211124 Carsonell
c 19	67.2	4.6	67970	3	PFMAL1P3	AL031746 Plasmodiu
c 20	67	4.6	130349	9	AC011593	AC011593 Homo sapi
c 21	67	4.6	198431	9	AC109994	AC109994 Homo sapi
c 22	66.8	4.5	97371	8	ATT28A8	AL162691 Arabidops
c 23	66.6	4.5	1141	6	AX083744	AX083744 Sequence
24	66.4	4.5	14635	3	AE001423	AE001423 Plasmodiu
c 25	66.4	4.5	18624	6	AX346604	AX346604 Sequence
26	66.4	4.5	30726	2	AC117269	AC117269 Dictyoste
27	66.2	4.5	1192	9	HS3323759	AJ323759 Homo sapi
c 28	66.2	4.5	115489	2	AE001398	AE001398 Plasmodiu
29	66.2	4.5	14867	3	AC117072	AC117072 Dictyoste
c 30	66.2	4.5	133148	9	AC009435	AC009435 Homo sapi
c 31	66	4.5	17538	6	AX346059	AX346059 Sequence
c 32	66	4.5	201299	9	AC007158	AC007158 Homo sapi
c 33	65.8	4.5	156060	2	AC004153	AC004153 Plasmodiu
c 34	65.6	4.5	7584	6	AX286935	AX286935 Sequence
c 35	65.4	4.4	22977	9	AC106883	AC106883 Homo sapi
c 36	65.4	4.4	162515	9	AC107032	AC107032 Homo sapi
c 37	65.2	4.4	23676	2	AC115599	AC115599 Dictyoste
c 38	65.2	4.4	124820	2	AC117073	AC117073 Dictyoste
c 39	65.2	4.4	141017	2	AC116962	AC116962 Dictyoste
c 40	65.2	4.4	165260	9	AC024341	AC024341 Homo sapi
c 41	65	4.4	43993	2	AC116965	AC116965 Dictyoste
42	65	4.4	165059	9	AC106856	AC106856 Homo sapi
c 43	65	4.4	321003	2	PFMAL4P3	AL035476 Plasmodiu
c 44	64.8	4.4	1141	6	AX083744	AX083744 Sequence
c 45	64.8	4.4	5884	6	AX347067	AX347067 Sequence

## ALIGNMENTS

RESULT 1  
AX154641  
LOCUS AX154641 1470 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1 from Patent WO0138550.  
ACCESSION AX154641  
VERSION AX154641.1 GI:14536200  
KEYWORDS  
SOURCE  
ORGANISM  
Candida albicans.  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Patent: WO 0138550-A 1 31-MAY-2001;  
Methods for altering the expression of hyphal-specific genes  
1 (bases 1 to 1470)  
Sundstrom,P.

Pred. No. is the number of results predicted by chance to have a





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RESULT 4
CAC35A5/c
LOCUS      CAC35A5 42565 bp DNA linear PLN 05-NOV-1998
ACCESSION AL033396
VERSION    AL033396.1 GI:3850143
KEYWORDS   chsl; CDP-alcohol phosphatidyltransferase; chitin synthase;
            chsl; cytochrome p450; DNA polymerase delta; histidine kinase;
            isocitrate dehydrogenase pseudogene; LTR; pol3; Rccl; regulator of
            chromosome condensation; rehydrin; RPS1-like region.
SOURCE     Candida albicans
ORGANISM   Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE  1 (bases 1 to 42565)
            Tait,E., Simon,M.C., King,S., Brown,A.J., Gow,N.A. and Shaw,D.J.
            A Candida albicans genome project: cosmid contigs, physical
            mapping, and gene isolation
            Fungal Genet. Biol. 21 (3), 308-314 (1997)
JOURNAL    97435544
MEDLINE    9290243
REMARK     Article No. FG970983
REFERENCE  2 (bases 1 to 42565)
            Oliver,K. and Harris,D.
            Unpublished
JOURNAL
REFERENCE  3 (bases 1 to 42565)
            Barrell,B.G. and Rajandream,M.A.
            Direct Submission
AUTHORS
TITLE      Submitted (05-NOV-1998) On behalf of the pilot sequencing project
            on the Candida albicans strain 1161 genome. Sanger Centre, Wellcome
            Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:
            barrellesanger.ac.uk Cosmids supplied by Prof. Duncan Shaw, [3]
            Department of Molecular and Cell Biology, The Institute of Medical
            Science, University of Aberdeen, Foresterhill, Aberdeen, AB25 22D,
            UK
COMMENT
Notes:
Funding: sequencing funded by Beowulf Genomics Ltd. CDS are
numbered using the following system eg CAC20C1.01c. CA (C.
albicans), 20C1 (cosmid name),
.01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE/PFAM
database are also included but some of these may be fortuitous.
IMPORTANT: This sequence MAY NOT be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions. Cosmid CAC35A5 is
likely to map to region R, chromosome 7.
Location/Qualifiers
1. .42565
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/strain="1161"
/db_xref="taxon:5476"
/map="chromosome 7"
/clone="cosmid CAC35A5"
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/gene="Ca35A5.01c"
complement(<1..785)
/gene="Ca35A5.01c"
/note="Ca35A5.01c, partial orf, len: > 261 aa, most
similar to EPTL_YEAST ethanolaminophosphotransferase (EC
2.7.8.1) (391 aa), fasta scores opt: 984, E(): 0, (56.3%
identity in 263 aa overlap), contains PS00379 CDP-alcohol
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/db_xref="GI:3850144"
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EYHTHTLFLSPGVEGILMICIIVITIGFIPDIWTIDLFELNLTLGLGYGYKVD
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/note="RPS1-like region"
complement(7606..8085)
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13175..14713
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/note="Ca35A5.02, unknown, len: 512 aa, possible
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KLNSNTSPSSNLTNTNTNTNALSRLFRNKSLSNI SVHPSSDDSSPKTLRESTSP
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TKPKKSSSPMSTFSLHFRSHHNSLNQDRTNQVATGTPPLSGKDFDFSKAKRT
LCLSSNSNIIISNPELAQIYFTNPNTIEDRETNLDHTNNSDLHKKMLVPADSF
IQNKLYHQTEVGLIGIYESLDHNDNKIYNLYHYLKLPLTFPSISDGGQSKMR
PILSASVEEIANVKESFCLHOPNHERSFRKSVSSLSGRKDRKVEDVYQLSNLFE
KLMSLHNLOTPESEVSLQALILNAKYNNAVYFVLLSIFOPLOIYLNELFTRSH
NGSKIIRIDDLVLSFRKVFTEQIGSGERETSQFLGNAESEDLTNGLLTSLAVL
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EMNKLRLVDQAARLVEFDKWCIFGPELKKIRRKVV"
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20719..21001
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20808..23888
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/note="Ca35A5.04, Chsl gene, len: 1026 aa, CHSL_CANAL
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(99.9% identity in 776 aa overlap) but open reading frame
here extends 250 aa upstream of CHSL_CANAL start
at 21561"
/codon_start=1
/transl_table=12
/product="chitin synthase"
/protein_id="CAA21947.1"

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REFERENCE 3 (bases 1 to 164399)  
 LAWSON, D., Bowman, S. and Barrell, B.  
 TITLE Submission  
 JOURNAL Submitted (14-AUG-1997) P.falciparum Genome Sequencing Consortium,  
 The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge  
 CB10 1SA, UK

COMMENT On or before May 14, 2001 this sequence version replaced  
 gi:2665320, gi:2982570, gi:2982576, gi:2894503, gi:2982580,  
 gi:2894373, gi:2982530.  
 For more information about this sequence or the Malaria Project,  
 see [http://www.sanger.ac.uk/Projects/P\\_falciparum](http://www.sanger.ac.uk/Projects/P_falciparum).

FEATURES  
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 aa, predicted using hexExon"  
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 complement(156..161)  
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 ORKICFENKTRRNRYFYDGENYKVAKNTSLIATNGRVKFFHVIQNVFLYNIL  
 PEELELKQDLYRYTEHVKSFEENRSLIYLRMKNILFPKIKQFYIRPKLPQFL  
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 DNTSYHNVPDFDVKCYKREKLYFMSKLYTCMIYCCYILIKNKIYIDPFCLY  
 LLLKSYFFIDTIINKYIYLPNPTCHKKFLRLFLLCNICTNFKDNTNINYEERIQ

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 INSIVNYGALPQYIEPKHIIYQNKSKKALLFTGNDPLDILDIGSLACKLGQV  
 PVKILGATFLIDEGLDVKI IAINKDKHYEDINSLDSIEKYIETHLLEWFRSYK  
 MADYTKNLISQLYDKSEDLIMTKHHYLFREFDVKYKLEHSEKTEKHEHYVNA  
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gene  
 CDS

misc\_feature  
 gene  
 CDS

Db	145856	ATAGCATATTTAATAGATAAATAAAATCATAAATTTATTTTGGTAAAAAATATT	145915
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Db	145916	AAAAAAAATATTAATTAAGGAATATATATAAAGAAATTAATTTGATPAAAAAGTTGG	145975
QY	1048	CTCATAAATCGCTTAAATATGTAACCTCTAAAGTAATCTAAAAACAACAACCTTTCTCAAAA	1107
Db	145976	ACATAAAAGGGGAATGATCAAAATATTAAAAAAATAAAGAAATATATATATATATATGTA	146035
QY	1108	CTATATAATTAATTAACCTAATGGCTCACACCGGGGATAAGTTAGTTCAGCCAGTGT	1167
Db	146036	CATACATATTTGTGCTGGTTTAAACAAACAGTTACATTTTAAATAATTTTAAATTTTTC	146095
QY	1168	TTTTTGCCTTA - TTTTATGACTACATTTTGTTCACTTTTTTTGGTGCAGCTTTAATACC	1225
Db	146096	ATTTTCTTAAGCTTTTTTTTTTGTGTTTTTCTTCATATTTCTTGTGTTTTCAGCAGAC	146155
QY	1226	GTTTTGAACACTTCTTTGATCACCTGTATCGCGCTTTTAAACATAGCAACTCTTCT	1285
Db	146156	ATTTTCTCAACTTTTCTTTTCTTCTTGAATCTTTTTCGTTTTTTTCTTTCGCAAT	146215
QY	1286	AAAGTCCCTTTCTTTCCCACTATTTTATCATCTCTGAAATATGTAATCAGAAATAGTTTT	1345
Db	146216	TCTCTCAATCTCTGTTTCTTTTGTATATCATCTTTTCAACCATATATCTTAATTTTTT	146275
QY	1346	TCAAAAACTATAAAT	1360
Db	146276	ACAATATCTTAAT	146290

RESULT 11	PFMAL3P4	113880 bp	DNA	linear	INV 29-APR-2000
LOCUS	Plasmodium falciparum MAL3P4, complete sequence.				
DEFINITION	AL008970 AL319179				
ACCESSION	AL008970.3	GI:7672212			
VERSION	HTG.				
KEYWORDS	Plasmodium falciparum 3D7,				
SOURCE	Plasmodium falciparum 3D7.				
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
REFERENCE	1 (bases 1 to 113880)				
AUTHORS	Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T., Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S., Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J., Moulé,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A., Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and Barrell,B.G.				
TITLE	The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum				
JOURNAL	Nature 400 (6744), 532-538 (1999)				
MEDLINE	99376085				
PUBMED	10448855				
REFERENCE	2 (bases 1 to 113880)				
AUTHORS	Hamlin,N., Bowman,S., Churcher,C., Lawson,D., Quail,M. and Barrell,B.				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 113880)				
AUTHORS	Lawson,D., Bowman,S. and Barrell,B.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-NOV-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK				
COMMENT	On Apr 30, 2000 this sequence version replaced gi:4493924. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.				
FEATURES	Location/Qualifiers				
source	1. .113880 /organism="Plasmodium falciparum 3D7" /strain="3D7" /db xref="taxon:36329"				

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misc_feature
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CDS"
2364. .6248
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2364. .6248
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/notes="PFC0435w (MAL3p4.26), Hypothetical protein, len:
1294 aa, predicted using hexExon"
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 The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum  
 Nature 400 (6744), 532-538 (1999)  
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 2 (bases 1 to 253305)  
 Oliver, K., Bowman, S., Harris, D., Lawson, D., Quail, M. and Barrell, B. Unpublished  
 3 (bases 1 to 253305)  
 Lawson, D., Bowman, S. and Barrell, B. Direct Submission  
 Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK  
 On or before May 14, 2001 this sequence version replaced  
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 For more information about this sequence or the Malaria Project, see [http://www.sanger.ac.uk/Projects/P\\_falciparum](http://www.sanger.ac.uk/Projects/P_falciparum).  
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